RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
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Application Serial Number: _09/845, 157 B_

Source: _JFWO_

Date Processed by STIC: _08/01/2003_

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IFW16

RAW SEQUENCE LISTING   DATE: 08/01/2005
PATENT APPLICATION: US/09/845,157B   TIME: 16:16:15

Input Set : A:\Sequence Listing ASCII, Docket No. 0942.5040001.ST25.txt
Output Set: N:\CRF4\08012005\I845157B.raw

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 5 <110> APPLICANT: Smith, Michael D.
 6        Potter, Robert J.
 7        Dhariwal, Gulshan
 8        Gerard, Gary F.
 9        Rosenthal, Kim
11 <120> TITLE OF INVENTION: Thermostable Reverse Transcriptases and Uses Thereof
13 <130> FILE REFERENCE: 0942.5040001/RWE/AWL
15 <140> CURRENT APPLICATION NUMBER: US 09/845,157B
16 <141> CURRENT FILING DATE: 2001-05-01
18 <150> PRIOR APPLICATION NUMBER: US 60/207,196
19 <151> PRIOR FILING DATE: 2000-05-26
22 <160> NUMBER OF SEQ ID NOS: 8
24 <170> SOFTWARE: PatentIn version 3.0
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 2151
29 <212> TYPE: DNA
30 <213> ORGANISM: Moloney-Murine Leukemia Virus
33 <220> FEATURE:
34 <221> NAME/KEY: CDS
35 <222> LOCATION: (1)..(2151)
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43 ggt gga cag caa atg ggt cgg gat ctg tac gac gat gac gat aag cat      96
44 Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys His
45             20                  25                  30
47 atg acc cta aat ata gaa gat gag tat cgg cta cat gag acc tca aaa     144
48 Met Thr Leu Asn Ile Glu Asp Glu Tyr Arg Leu His Glu Thr Ser Lys
49         35                  40                  45
51 gag cca gat gtt tct cta ggg tcc aca tgg ctg tct gat ttt cct cag     192
52 Glu Pro Asp Val Ser Leu Gly Ser Thr Trp Leu Ser Asp Phe Pro Gln
53     50                  55                  60
55 gcc tgg gcg gaa acc ggg ggc atg gga ctg gca gtt cgc caa gct cct     240
56 Ala Trp Ala Glu Thr Gly Gly Met Gly Leu Ala Val Arg Gln Ala Pro
57 65                  70                  75                  80
59 ctg atc ata ctt ctg aaa gca acc tct acc ccc gtg tcc ata aaa caa     288
60 Leu Ile Ile Leu Leu Lys Ala Thr Ser Thr Pro Val Ser Ile Lys Gln
61                 85                  90                  95
63 tac ccc atg tca caa gaa gcc aga ctg ggg atc aag ccc cac ata cag     336
64 Tyr Pro Met Ser Gln Glu Ala Arg Leu Gly Ile Lys Pro His Ile Gln
65             100                 105                 110
67 aga ctg ttg gac cag gga ata ctg gta ccc tgc cag tcc ccc tgg aac     384
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68 Arg Leu Leu Asp Gln Gly Ile Leu Val Pro Cys Gln Ser Pro Trp Asn
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71 acg ccc ctg cta ccc gtc aag aaa ccc ggg act aat gat tac agg cct      432
72 Thr Pro Leu Leu Pro Val Lys Lys Pro Gly Thr Asn Asp Tyr Arg Pro
73          130               135           140
75 gtc caa gat ctg aga gag gtc aac aaa cgc gta gaa gac atc cac ccc      480
76 Val Gln Asp Leu Arg Glu Val Asn Lys Arg Val Glu Asp Ile His Pro
77 145               150               155               160
79 acc gta ccc aac ccc tac aac ctc ttg agt ggg ctc cca ccg tcc cac      528
80 Thr Val Pro Asn Pro Tyr Asn Leu Leu Ser Gly Leu Pro Pro Ser His
81               165               170               175
83 cag tgg tac act gtt cta gac tta aaa gat gcc ttt ttc tgc ctg aga      576
84 Gln Trp Tyr Thr Val Leu Asp Leu Lys Asp Ala Phe Phe Cys Leu Arg
85               180               185           190
87 ctc cac ccg acg tct cag cct ctc ttc gcc ttt gaa tgg aga gac cca      624
88 Leu His Pro Thr Ser Gln Pro Leu Phe Ala Phe Glu Trp Arg Asp Pro
89          195               200               205
91 gag atg gga atc tct ggc caa cta acc tgg acc aga ctc cca cag gga      672
92 Glu Met Gly Ile Ser Gly Gln Leu Thr Trp Thr Arg Leu Pro Gln Gly
93          210               215           220
95 ttc aaa aac agt ccc acc ctg ttt gat gag gca ctg cgc aga gac cta      720
96 Phe Lys Asn Ser Pro Thr Leu Phe Asp Glu Ala Leu Arg Arg Asp Leu
97 225               230               235               240
99 gca gac ttc cgg atc cag cac cca gac ttg atc ctg cta cag tac gta      768
100 Ala Asp Phe Arg Ile Gln His Pro Asp Leu Ile Leu Leu Gln Tyr Val
101               245               250               255
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104 Asp Asp Leu Leu Leu Ala Ala Thr Ser Glu Leu Asp Cys Gln Gln Gly
105               260               265           270
107 act cgg gcc ctg tta caa acc cta gga gac ctc ggg tat cgg gcc tcg     864
108 Thr Arg Ala Leu Leu Gln Thr Leu Gly Asp Leu Gly Tyr Arg Ala Ser
109          275               280               285
111 gcc aag aaa gcc caa att tgc cag aaa cag gtc aag tat ctg ggg tat     912
112 Ala Lys Lys Ala Gln Ile Cys Gln Lys Gln Val Lys Tyr Leu Gly Tyr
113          290               295               300
115 ctt cta aaa gag ggt cag aga tgg ctg act gag gcc aga aaa gag act     960
116 Leu Leu Lys Glu Gly Gln Arg Trp Leu Thr Glu Ala Arg Lys Glu Thr
117 305               310               315               320
119 gtg atg ggg cag cct act ccg aag acc ccg cgg caa cta agg gag ttc    1008
120 Val Met Gly Gln Pro Thr Pro Lys Thr Pro Arg Gln Leu Arg Glu Phe
121               325               330               335
123 cta ggg acg gca ggc ttc tgt cgc ctc tgg atc cct ggg ttt gca gaa    1056
124 Leu Gly Thr Ala Gly Phe Cys Arg Leu Trp Ile Pro Gly Phe Ala Glu
125               340               345               350
127 atg gca gcc ccc ttg tac cct ctc acc aaa acg ggg act ctg ttt aat    1104
128 Met Ala Ala Pro Leu Tyr Pro Leu Thr Lys Thr Gly Thr Leu Phe Asn
129               355               360               365
131 tgg ggc cca gac caa caa aag gcc tat caa gaa atc aag caa gct ctt    1152
132 Trp Gly Pro Asp Gln Gln Lys Ala Tyr Gln Glu Ile Lys Gln Ala Leu
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135 cta act gcc cca gcc ctg ggg ttg cca gat ttg act aag ccc ttt gaa    1200
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137 385                   390                   395                   400
139 ctc ttt gtc gac gag aag cag ggc tac gcc aaa ggt gtc cta acg caa    1248
140 Leu Phe Val Asp Glu Lys Gln Gly Tyr Ala Lys Gly Val Leu Thr Gln
141                   405                   410                   415
143 aaa ctg gga cct tgg cgt cgg ccg gtg gcc tac ctg tcc aaa aag cta    1296
144 Lys Leu Gly Pro Trp Arg Arg Pro Val Ala Tyr Leu Ser Lys Lys Leu
145                   420                   425                   430
147 gac cca gta gca gct ggg tgg ccc cct tgc cta cgg atg gta gca gcc    1344
148 Asp Pro Val Ala Ala Gly Trp Pro Pro Cys Leu Arg Met Val Ala Ala
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151 att gcc gta ctg aca aag gat gca ggc aag cta acc atg gga cag cca    1392
152 Ile Ala Val Leu Thr Lys Asp Ala Gly Lys Leu Thr Met Gly Gln Pro
153       450                   455                   460
155 cta gtc att ctg gcc ccc cat gca gta gag gca cta gtc aaa caa ccc    1440
156 Leu Val Ile Leu Ala Pro His Ala Val Glu Ala Leu Val Lys Gln Pro
157 465                   470                   475                   480
159 ccc gat cga tgg ctt tcc aac gcc cgg atg act cac tat cag gcc ttg    1488
160 Pro Asp Arg Trp Leu Ser Asn Ala Arg Met Thr His Tyr Gln Ala Leu
161                   485                   490                   495
163 ctt ttg gac acg gac cgg gtc cag ttc gga ccg gtg gta gcc ctg aac    1536
164 Leu Leu Asp Thr Asp Arg Val Gln Phe Gly Pro Val Val Ala Leu Asn
165                   500                   505                   510
167 ccg gct aca ctg ctc cca ctg cct gag gaa ggg ctg cag cac aac tgc    1584
168 Pro Ala Thr Leu Leu Pro Leu Pro Glu Glu Gly Leu Gln His Asn Cys
169       515                   520                   525
171 ctt gat atc ctg gcc gaa gcc cac gga acc cga ccc gac cta acg gac    1632
172 Leu Asp Ile Leu Ala Glu Ala His Gly Thr Arg Pro Asp Leu Thr Asp
173       530                   535                   540
175 cag ccg ctc cca gac gcc gac cac acc tgg tac acg ggt gga tcc agt    1680
176 Gln Pro Leu Pro Asp Ala Asp His Thr Trp Tyr Thr Gly Gly Ser Ser
177 545                   550                   555                   560
179 ctc ttg caa gag gga cag cgt aag gcg gga gct gcg gtg acc acc gag    1728
180 Leu Leu Gln Glu Gly Gln Arg Lys Ala Gly Ala Ala Val Thr Thr Glu
181                   565                   570                   575
183 acc gag gta atc tgg gct aaa gcc ctg cca gcc ggg aca tcc gct cag    1776
184 Thr Glu Val Ile Trp Ala Lys Ala Leu Pro Ala Gly Thr Ser Ala Gln
185             580                   585                   590
187 cgg gct cag ctg ata gca ctc acc cag gcc cta agg atg gca gaa ggt    1824
188 Arg Ala Gln Leu Ile Ala Leu Thr Gln Ala Leu Arg Met Ala Glu Gly
189       595                   600                   605
191 aag aag cta aat gtt tat acg aat tcc cgt tat gct ttt gct act gcc    1872
192 Lys Lys Leu Asn Val Tyr Thr Asn Ser Arg Tyr Ala Phe Ala Thr Ala
193       610                   615                   620
195 cat atc cat gga gaa ata tac aga agg cgt ggg ttg ctc aca tca gaa    1920
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203 ctc ttt ctg ccc aaa aga ctt agc ata atc cat tgt cca gga cat caa      2016
204 Leu Phe Leu Pro Lys Arg Leu Ser Ile Ile His Cys Pro Gly His Gln
205             660             665             670
207 aag gga cac agc gcc gag gct aga ggc aac cgg atg gct gac caa gcg      2064
208 Lys Gly His Ser Ala Glu Ala Arg Gly Asn Arg Met Ala Asp Gln Ala
209         675             680             685
211 gcc cga aag gca gcc atc aca gag aat cca gac acc tct acc ctc ctc      2112
212 Ala Arg Lys Ala Ala Ile Thr Glu Asn Pro Asp Thr Ser Thr Leu Leu
213     690             695             700
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217 705             710             715
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221 <211> LENGTH: 716
222 <212> TYPE: PRT
223 <213> ORGANISM: Moloney-Murine Leukemia Virus
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236         35              40              45
238 Glu Pro Asp Val Ser Leu Gly Ser Thr Trp Leu Ser Asp Phe Pro Gln
239     50              55              60
241 Ala Trp Ala Glu Thr Gly Gly Met Gly Leu Ala Val Arg Gln Ala Pro
242 65              70              75              80
244 Leu Ile Ile Leu Leu Lys Ala Thr Ser Thr Pro Val Ser Ile Lys Gln
245             85              90              95
247 Tyr Pro Met Ser Gln Glu Ala Arg Leu Gly Ile Lys Pro His Ile Gln
248         100             105             110
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251         115             120             125
253 Thr Pro Leu Leu Pro Val Lys Lys Pro Gly Thr Asn Asp Tyr Arg Pro
254     130             135             140
256 Val Gln Asp Leu Arg Glu Val Asn Lys Arg Val Glu Asp Ile His Pro
257 145             150             155             160
259 Thr Val Pro Asn Pro Tyr Asn Leu Leu Ser Gly Leu Pro Pro Ser His
260             165             170             175
262 Gln Trp Tyr Thr Val Leu Asp Leu Lys Asp Ala Phe Phe Cys Leu Arg
263         180             185             190
265 Leu His Pro Thr Ser Gln Pro Leu Phe Ala Phe Glu Trp Arg Asp Pro
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269     210             215             220
271 Phe Lys Asn Ser Pro Thr Leu Phe Asp Glu Ala Leu Arg Arg Asp Leu
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280 Thr Arg Ala Leu Leu Gln Thr Leu Gly Asp Leu Gly Tyr Arg Ala Ser
281         275             280                 285
283 Ala Lys Lys Ala Gln Ile Cys Gln Lys Gln Val Lys Tyr Leu Gly Tyr
284     290                 295                 300
285 Leu Leu Lys Glu Gly Gln Arg Trp Leu Thr Glu Ala Arg Lys Glu Thr
286 305                 310                 315                 320
288 Val Met Gly Gln Pro Thr Pro Lys Thr Pro Arg Gln Leu Arg Glu Phe
289             325             330                 335
291 Leu Gly Thr Ala Gly Phe Cys Arg Leu Trp Ile Pro Gly Phe Ala Glu
292             340             345                 350
294 Met Ala Ala Pro Leu Tyr Pro Leu Thr Lys Thr Gly Thr Leu Phe Asn
295         355             360                 365
297 Trp Gly Pro Asp Gln Gln Lys Ala Tyr Gln Glu Ile Lys Gln Ala Leu
298     370                 375                 380
300 Leu Thr Ala Pro Ala Leu Gly Leu Pro Asp Leu Thr Lys Pro Phe Glu
301 385                 390                 395                 400
303 Leu Phe Val Asp Glu Lys Gln Gly Tyr Ala Lys Gly Val Leu Thr Gln
304             405                 410                 415
306 Lys Leu Gly Pro Trp Arg Arg Pro Val Ala Tyr Leu Ser Lys Lys Leu
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309 Asp Pro Val Ala Ala Gly Trp Pro Pro Cys Leu Arg Met Val Ala Ala
310         435                 440                 445
312 Ile Ala Val Leu Thr Lys Asp Ala Gly Lys Leu Thr Met Gly Gln Pro
313     450                 455                 460
315 Leu Val Ile Leu Ala Pro His Ala Val Glu Ala Leu Val Lys Gln Pro
316 465             470                 475                 480
318 Pro Asp Arg Trp Leu Ser Asn Ala Arg Met Thr His Tyr Gln Ala Leu
319             485                 490                 495
321 Leu Leu Asp Thr Asp Arg Val Gln Phe Gly Pro Val Val Ala Leu Asn
322             500                 505                 510
324 Pro Ala Thr Leu Leu Pro Leu Pro Glu Glu Gly Leu Gln His Asn Cys
325         515                 520                 525
327 Leu Asp Ile Leu Ala Glu Ala His Gly Thr Arg Pro Asp Leu Thr Asp
328     530                 535                 540
330 Gln Pro Leu Pro Asp Ala Asp His Thr Trp Tyr Thr Gly Gly Ser Ser
331 545             550                 555                 560
333 Leu Leu Gln Glu Gly Gln Arg Lys Ala Gly Ala Ala Val Thr Thr Glu
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336 Thr Glu Val Ile Trp Ala Lys Ala Leu Pro Ala Gly Thr Ser Ala Gln
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343 Lys Lys Leu Asn Val Tyr Thr Asn Ser Arg Tyr Ala Phe Ala Thr Ala
344     610                 615                 620
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 08/01/2005
PATENT APPLICATION: **US/09/845,157B**   TIME: 16:16:16

Input Set : **A:\Sequence Listing ASCII, Docket No. 0942.5040001.ST25.txt**
Output Set: **N:\CRF4\08012005\I845157B.raw**

Invalid <213> Response:
Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:3,4,5

VERIFICATION SUMMARY   DATE: 08/01/2005
PATENT APPLICATION: **US/09/845,157B**   TIME: 16:16:16

Input Set : **A:\Sequence Listing ASCII, Docket No. 0942.5040001.ST25.txt**
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